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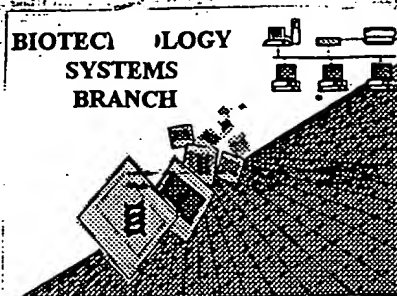
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RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0420
0470
2/21/01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/734,237

Source: OIPE

Date Processed by STIC: 12-19-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/734,237

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) possibly All are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

DATE: 12/19/2000

TIME: 07:26:16

Output Set: N:\CRF3\12192000\I734237.raw

Does Not Comply
Corrected Diskette Needed

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3 <110> APPLICANT: Rozzell, J. David
4 Bui, Peter
5 Hua, Ling
7 <120> TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
9 <130> FILE REFERENCE: B583:40608
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/734,237
C--> 11 <141> CURRENT FILING DATE: 2000-12-02
11 <150> PRIOR APPLICATION NUMBER: 09/494,921
12 <151> PRIOR FILING DATE: 2000-01-31
14 <160> NUMBER OF SEQ ID NOS: 79
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1197
20 <212> TYPE: DNA
21 <213> ORGANISM: Pseudomonas putida
23 <400> SEQUENCE: 1
24 atgcacgqct ccaacaagct cccaggattt gccaccgcgc ccattnacca tggctacgac 60
26 ccccaggacc acggcggcgc actggtgcc aagggtctacc agaccgcgac gttcaccttc 120
28 cccaccgttg aatacgcgcg tgcgtgcttt gccgcgcgac aggcgcggca ttctacagc 180
30 cgcattccca accccacct caacctgtg gaagcacgca tggcctcgcl ggaaggcggc 240
32 gaggcggggc tggcgctgca ctgcggcgat gggggcgatca cgtccacgct atgggacaatg 300
34 ctgcgcgccg gtgacgaggt gctgctgggc aacacctgt acgactgcac ctttgccttc 360
36 ctgcaccacc gcatcgcgga gttcggggtc aagctgcgcc atgtggacat ggccgacctg 420
38 caggcactgg aggcggccal gacgcgggcc acccggtga tctattcga tgcgcgggcc 480
40 aaccccaaca tgcacatggc cgtatcgcc ggcgtggcga agattgcac caagcacggc 540
42 cgcacccgtg tggtcgacaa cactactgc acgcggtacc tgcgacggcc actggagctg 600
44 ggcgcgacc tggttggcga ttgcgccacc aagtacctga gcggccatg cgacatcaat 660
46 gctggcattg tgggtggcag ccaggcactg gtggacgcta tacgtctgca gggcctcaag 720
48 gacatgacgg gtgcgggtct ctgcgcccat gacgcgcgac tgttgatgcy cggcatcaag 780
50 accctcaacc tgcgcattga cgcgcaatgc gccaacgctc aggtgtctgc caggttcttc 840
52 ggcgcgagc cgcaggttga ctgtatccat tacccgggcc ttgcgagctt ccgcagctac 900
54 accctggccc gccagcagat gagccagccg ggcggcatga tgcctctcga actcaagggc 960
56 gtcacgcgtg cggggcgggc gttcatgaac gccctgcaac tgttcagcgc cgcggtgagc 1020
58 ctggcgcatg ccgagtcgct ggcgcagcac ccggcaagca tgactcaatc cagctatacc 1080
60 ccaggaggag gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg 1140
62 gaagacatcy acgacctgct ggcgcatgtg caacaggcac tcaaggcgag tgcctgca 1197
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 399
67 <212> TYPE: PRN
68 <213> ORGANISM: Artificial Sequence
W--> 70 <220> FEATURE:
W--> 70 <223> OTHER INFORMATION:
70 <400> SEQUENCE: 2
72 Met Gly His Gly Ser Asn Lys Leu Pro Gly Phe Ala Thr Arg Ala Ile
73 1 5 10 15 the
75 His His Gly Tyr Asp Pro Gln Asp His Gly Gly Ala Leu Val Pro Pro
76 20 25 30 ca

```

missing Mandatory <220> and
<223> features to explain
the source of the
genetic material in
the artificial sequence.
See #12 on the Error
Summary Sheet.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/734,237

DATE: 12/19/2000
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Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\12192000\I734237.raw

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78 Val Tyr Gln Thr Ala Thr Phe Thr Phe Pro Thr Val Glu Tyr Gly Ala
79          35          40          45
81 Ala Cys Phe Ala Gly Gln Gln Ala Gly His Pro Tyr Ser Arg Ile Ser
82          50          55          60
84 Asn Pro Thr Leu Asn Leu Leu Gln Ala Arg Met Ala Ser Leu Glu Gly
85 65          70          75          80
87 Gly Glu Ala Gly Leu Ala Leu Ala Ser Gly Met Gly Ala Ile Thr Ser
88          85          90          95
90 Thr Leu Tyr Thr Leu Leu Arg Pro Gly Asp Glu Val Leu Leu Gly Asn
91          100          105          110
93 Thr Leu Tyr Gly Cys Thr Phe Ala Phe Leu His His Gly Ile Gly Glu
94          115          120          125
96 Phe Gly Val Lys Leu Arg His Val Asp Met Ala Asp Leu Gln Ala Leu
97          130          135          140
99 Glu Ala Ala Met Thr Pro Ala Thr Arg Val Ile Tyr Phe Glu Ser Pro
100 145          150          155          160
102 Ala Asn Pro Asn Met His Met Ala Asp Ile Ala Gly Val Ala Lys Ile
103          165          170          175
105 Ala Arg Lys His Gly Ala Thr Val Val Val Asp Asn Thr Tyr Cys Thr
106          180          185          190
108 Pro Tyr Leu Gln Arg Pro Leu Gln Leu Gly Ala Asp Leu Val Val His
109          195          200          205
111 Ser Ala Thr Lys Tyr Leu Ser Gly His Gly Asp Ile Thr Ala Gly Ile
112          210          215          220
114 Val Val Gly Ser Gln Ala Leu Val Asp Arg Ile Arg Leu Glu Gly Leu
115 225          230          235          240
117 Lys Asp Met Thr Gly Ala Val Leu Ser Pro His Asp Ala Ala Leu Leu
118          245          250          255
120 Met Arg Gly Ile Lys Thr Leu Asn Leu Arg Met Asp Arg His Cys Ala
121          260          265          270
123 Asn Ala Gln Val Leu Ala Glu Phe Leu Ala Arg Gln Pro Gln Val Glu
124          275          280          285
126 Leu Ile His Tyr Pro Gly Leu Ala Ser Phe Pro Gln Tyr Thr Leu Ala
127          290          295          300
129 Arg Gln Gln Met Ser Gln Pro Gly Gly Met Ile Ala Phe Glu Leu Lys
130 305          310          315          320
132 Gly Gly Ile Gly Ala Gly Arg Arg Phe Met Asn Ala Leu Gln Leu Phe
133          325          330          335
135 Ser Arg Ala Val Ser Leu Gly Asp Ala Glu Ser Leu Ala Gln His Pro
136          340          345          350
138 Ala Ser Met Thr His Ser Ser Tyr Thr Pro Glu Glu Arg Ala His Tyr
139          355          360          365
141 Gly Ile Ser Glu Gly Leu Val Arg Leu Ser Val Gly Leu Glu Asp Ile
142          370          375          380
144 Asp Asp Leu Leu Ala Asp Val Gln Gln Ala Leu Lys Ala Ser Ala
145 385          390          395
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 1202
149 <212> TYPE: DNA

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RAW SEQUENCE LISTING
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Input Set : A:\B583_40608.txt
Output Set: H:\CRF3\12192000\I734237.raw

150 <213> ORGANISM: Artificial sequence
W--> 152 <220> FEATURE:
W--> 152 <223> OTHER INFORMATION: *Same, refer to p.1*
152 <400> SEQUENCE: 3
153 catgggtcac ggtcccaaca aactgccggg ctttgcctacc cgcgctatcc accacgggta 60
155 tgacccgcag gatcacgggt gtgcactggt tccgccgggt taccagactg ctactttcac 120
157 ctcccgacc gttgaatacg gcgctgcgtg ctttgcctggc gaacaggtcg gtcacttcta 180
159 ctcccgatc tccaacccga cctggaacct gctggaagca cgtatggcat ctctggaagg 240
161 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta cctgtgggac 300
163 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatgggt gtacttttgc 360
165 ttctctgcac caccgtatcg gtgaattcgg cgttaaactg cgtcagctag atatggctga 420
167 cctgcaggca ctggaaagcg ctatgacccc ggtacccgtt gttatctact tcgaatcccc 480
169 ggttaacccg aacatgcaca tggctgacat cgcaggtgtt gctaaactcg ctctgaagca 540
171 cgcgctacc gtagttggtg ataacaccta ctgtactcgc taccctgcaac gtcgctgga 600
173 actgggcgct gaacctggtt ttactcgcg tactaaatag ctgtccggcc acggcgacat 660
175 cactgctgac atcgtatgag gctcccgagg actggttgac cgtatccgct tgcgaagctc 720
177 gaaagacatg accggcgctg ttctgtcccc qcacgacgca gcactgctga tgcgtggtat 780
179 caagacctg aacctgcgta tggaccgtca ctgtgctaac gctcaggtac tggctgaatt 840
181 cctggctcgt cagccgcagg tagaartgat ccaactatcc ggcctggctt ccttcccgca 900
183 gtacactctg qcacgtcagc agatgtccca gccgggcggg atgactcgtt tcgaactgaa 960
185 ggggtgcatc ggcgctgggt gtcgtttcat gaacgtctcg cagctgttct cccgtgcggt 1020
187 ttccclgggt gaacgtgaat ccttggcgca gcacccgca tccatgactc actcctcta 1080
189 cactccggaa gacgtgcgc actacgcat ctcggaaggc ctggttcgct tgtctgttgg 1140
191 tctggaagac atcgatgatc tgcctggcaga cgttcagcag gctctgaagg ctacgcttg 1200
193 ag 1202
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 426
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial sequence
W--> 201 <220> FEATURE:
W--> 201 <223> OTHER INFORMATION: *Same*
201 <400> SEQUENCE: 4
202 catgggtcac ggtcccaaca aactgccggg ctttgcctacc cgcgctatcc accacgggta 60
204 tgacccgcag gatcacgggt gtgcactggt tccgccgggt taccagactg ctactttcac 120
206 ctcccgacc gttgaatacg gcgctgcgtg ctttgcctggc gaacaggtcg gtcacttcta 180
208 ctcccgatc tccaacccga cctggaacct gctggaagca cgtatggcat ctctggaagg 240
210 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta cctgtgggac 300
212 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatgggt gtacttttgc 360
214 ttctctgcac caccgtatcg gtgaattcgg cgttaaactg cgtcagctag atatggctga 420
216 cctgca 426
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 441
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial sequence
W--> 224 <220> FEATURE:
W--> 224 <223> OTHER INFORMATION: *Same*
224 <400> SEQUENCE: 5
225 caagaggcca tgggtcacgg ctccaacaaa ctgccgggct ttgctaccgg cgctatccac 60
227 cagcgttatg accgcagga tcacgggtgt gcactggttc cgcgggtlla ccagactgct 120

RAW SEQUENCE LISTING
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Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\12192000\I734237.raw

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229 actttacact tcccgaccgt tgaatacggc gctgcgtgct ttgctggcga acaggctggt 180
231 cactttactt cccgtatctc caaccgcacc ctgaacctgc tgggaagcag tatggcatct 240
233 ctggaagggc gcaagactgg tctggcctg qcatctgta tgggcgcgat cactctacc 300
235 ctgtggacc tctgtgcgtc ggtgacgaa gttctgctgg qcaacacct gtatggttgt 360
237 acttttgcct tcccgacca cgtatcggg gaattcggcg ttaacctgcy tcaagtagat 420
239 atggctgacc tgcaggcaat g 441
242 <210> SEQ ID NO: 6
243 <211> LENGTH: 410
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial sequence
W--> 247 <220> FEATURE:
W--> 247 <223> OTHER INFORMATION:
247 <400> SEQUENCE: 6
248 ggcactggaa gcggctatga ccccggtac cctgtttatc tacttcgaat ccccggttaa 60
250 cccgaacatg cacatggctg acatcgacg tgttgctaaa atcgctcgt aycacggcgc 120
252 taccgtagtt gttgataaca cctactgtac tccgtacctg caacgtccgc tggaaactgg 180
254 cgttgacctg gttgttcacl cctgtactaa atacctgtcc ggcacggcg acatcactgc 240
256 tggcatcgta gtaggtccc aggcactggt tgacctatc cgtctgcaag gtctgaaaga 300
258 catgaccggc gctgttctgt ccccgacga cgcagcactg ctgatgcgtg gtatcaagac 360
260 cctgaacctg cgtatggacc gtcactgtgc taacgtccag gtactggctg 410
263 <210> SEQ ID NO: 7
264 <211> LENGTH: 430
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial sequence
W--> 268 <220> FEATURE:
W--> 268 <223> OTHER INFORMATION:
268 <400> SEQUENCE: 7
269 gctgacctgc aggcactgga agcggctatg acccggteta cccgtgttat ctacttcgaa 60
271 tcccggtcta accgaacat gcacatggct gacatcgag gtgttgctaa aatcgctcgt 120
273 aagcagggcg ctaccgtagt tgttgataac acctactgta ctcctgacct gcaacgtccg 180
275 ctggaactgg gcgctgaact ggttgttcacl tccgctacta aatacctgtc cggccacggc 240
277 gacatcactg ctggcatcgt agtaggtcc caggcactgg ttgacctat cctgtgcaa 300
279 ggtctgaaag acatgaccgg cgtgttctg tcccgacag acgcagcact gctgatgcgt 360
281 ggtatcaaga cctgaacct gcgtatggac cgtcactgtg ctaacgtca ggtactggct 420
283 gaattcctgg 430
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 366
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial sequence
W--> 291 <220> FEATURE:
W--> 291 <223> OTHER INFORMATION:
291 <400> SEQUENCE: 8
292 aattcctggc tcttcagccg caggtagaac tgatccacta tccgggacct gcttccctcc 60
294 cgcagtacac tctggcacgt cagcagatgt cccagccggg cggatagatc gctttcgaac 120
296 tgaaggggtg calcgcgct ggtcgtcgtt tcatgaacgc tctgcagctg ttctcccgty 180
298 cggtttccct ggttgacgt gaatecctgg cgcagcacc ggcacccatg actcactcct 240
300 cctacactcc ggaagaaagt gcgcactacg geatctccga aggcctggtt cgtctgtctg 300
302 ttggtctgga agacatcgt gatctgctgg cagacgttca gcaggctctg aaggctagcg 360
304 cttyag 366

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Some, refer to p1

Same

Same

RAW SEQUENCE LISTING DATE: 12/19/2000
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Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\12192000\I734237.raw

307 <210> SEQ ID NO: 9
 308 <211> LENGTH: 383
 309 <212> TYPE: DNA
 310 <213> ORGANISM: Artificial Sequence
 W--> 312 <220> FEATURE: *—————> Same, refer to p.1*
 W--> 312 <223> OTHER INFORMATION:
 312 <400> SEQUENCE: 9
 313 tcttaaatgaa ttcttggtc gtcagccgca ggtagaacty atccactatc cgggacctggc 60
 315 ttccctcccg cagtacactc tggcacytca gcagatgtcc cagccgggcg gtatgatcgc 120
 317 ttctgaacty aagggtggca tcggcgctgg tctctgttcc atgaacgctc tgcagctgtt 180
 319 ctcccggtgcg gtttccctgg gtgacgctga atccctggcg cagcaccggy catccatgac 240
 321 tcaactctcc tacactccgg aagaacgtgc gcactacggc atctccgaag gcttggttcg 300
 323 tctgtctgtt ggtctggaag acatcgatga tctgctggca gacgttcagc aggtcttgaa 360
 325 ggctaagcgt tgaggatcca cca 383
 326 <210> SEQ ID NO: 10
 329 <211> LENGTH: 33
 330 <212> TYPE: DNA
 331 <213> ORGANISM: Artificial Sequence
 W--> 333 <220> FEATURE: *—————> Same*
 W--> 333 <223> OTHER INFORMATION:
 333 <400> SEQUENCE: 10
 334 caagaggcca tgggtcacgg ctccaacaaa ctg 33
 337 <210> SEQ ID NO: 11
 338 <211> LENGTH: 114
 339 <212> TYPE: DNA
 340 <213> ORGANISM: Artificial Sequence
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 W--> 342 <223> OTHER INFORMATION:
 342 <400> SEQUENCE: 11
 343 caaggctcca aaaaactgcc gggctttgct acccgcgcta tccaccaagg ttatgacccg 60
 345 caggatcacg gttgtgcact ggttccgcg gtttaccaga ctgtactttt cacc 114
 348 <210> SEQ ID NO: 12
 349 <211> LENGTH: 116
 350 <212> TYPE: DNA
 351 <213> ORGANISM: Artificial Sequence
 W--> 353 <220> FEATURE: *—————> Same*
 W--> 353 <223> OTHER INFORMATION:
 353 <400> SEQUENCE: 12
 354 gcttccagca ggttcagggt cgggttggag atacgggagt agaagtgacc agcctgttgc 60
 356 ccagcaaaagc acgcagcgcc gtattcaacg gtcgggaagg tgaagtagc agtctg 116
 359 <210> SEQ ID NO: 13
 360 <211> LENGTH: 117
 361 <212> TYPE: DNA
 362 <213> ORGANISM: Artificial Sequence
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 W--> 364 <223> OTHER INFORMATION:
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 367 gcatacggta tgggcgcgat caccctacc ctgtggacc ttctgcgtcc gggtagc 117

← F.Y.I.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY DATE: 12/19/2000
PATENT APPLICATION: US/09/734,237 TIME: 07:26:17

Input Set : A:\B583_40608.txt
Output Set: N:\CRF3\12192000\I734237.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:70 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:152 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:152 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:201 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:201 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:224 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:224 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:247 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:247 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:268 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:268 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/734,237

DATE: 12/19/2000

TIME: 07:26:17

Input Set : A:\B583_40608.txt

Output Set: H:\CRF3\12192000\I734237.raw

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